

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Griffeth, Irwin J.;
Pollock, Joanne;
Bond, Julian F.;
Garman, Richard D;
Kuo, Mei-Chang;
Yeung, Siu-mei H.;
Brauer, Andrew;
Exley, Mark A.;
Powers, Steven P.
- (ii) TITLE OF INVENTION: Allergenic Proteins And Peptides From
Japanese Cedar Pollen
- (iii) NUMBER OF SEQUENCES: 201
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc.
(B) STREET: 610 Lincoln St
(C) CITY: Waltham
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02154
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US93/00139
(B) FILING DATE: January 15, 1993
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/938,990
(B) FILING DATE: September 1, 1992
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Darlene A. Vanstone
(B) REGISTRATION NUMBER: 35,729
(C) REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028PC)
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 466-6000
(B) TELEFAX: (617) 466-6040

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Crytpomeria japonica
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 66..1187
- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 129 1187

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Griffith, Irwin J. et al.

(ii) TITLE OF INVENTION: Allergenic Proteins And Peptides From
Japanese Cedar Pollen

(iii) NUMBER OF SEQUENCES: 195

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
(B) STREET: 610 Lincoln Street
(C) CITY: Waltham
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02154

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/M9-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Darlene A. Vanstone
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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1337 base pairs
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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Crytpomeria japonica

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 66..1187

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 129..1187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	AGTCAATCTG CTCATAATCA TAGCATAGCC GTATAGAAAG AAATTCTACA CTCTGCTACC	60
5	AAAAA ATG GAT TCC CCT TGC TTA GTA GCA TTA CTG GTT TTC TCT TTT Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe -21 -20 -15 -10	107
10	GTA ATT GGA TCT TGC TTT TCT GAT AAT CCC ATA GAC AGC TGC TGG AGA Val Ile Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg -5 1 5	155
15	GGA GAC TCA AAC TGG GCC CAA AAT AGA ATG AAG CTC GCA GAT TGT GCA Gly Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala 10 15 20 25	203
20	GTG GGC TTC GGA AGC TCC ACC ATG GGA GGC AAG GGA GGA GAT CTT TAT Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr 30 35 40	251
25	ACG GTC ACG AAC TCA GAT GAC GAC CCT GTG AAT CCT GCA CCA GGA ACT Thr Val Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr 45 50 55	299
30	CTG CGC TAT GGA GCA ACC CGA GAT AGG CCC CTG TGG ATA ATT TTC AGT Leu Arg Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser 60 65 70	347
35	GGG AAT ATG AAT ATA AAG CTC AAA ATG CCT ATG TAC ATT GCT GGG TAT Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr 75 80 85	395
40	AAG ACT TTT GAT GGC AGG GGA GCA CAA GTT TAT ATT GGC AAT GGC GGT Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly 90 95 100 105	443
45	CCC TGT GTG TTT ATC AAG AGA GTT AGC AAT GTT ATC ATA CAC GGT TTG Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu 110 115 120	491
50	TAT CTG TAC GGC TGT AGT ACT AGT GTT TTG GGG AAT GTT TTG ATA AAC Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn 125 130 135	539
55	GAG AGT TTT GGG GTG GAG CCT GTT CAT CCT CAG GAT GGC GAT GCT CTT Glu Ser Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu 140 145 150	587
60	ACT CTG CGC ACT GCT ACA AAT ATT TGG ATT GAT CAT AAT TCT TTC TCC Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser 155 160 165	635
65	AAT TCT TCT GAT GGT CTG GTC GAT GTC ACT CTT ACT TCG ACT GGA GTT Asn Ser Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val 170 175 180 185	683
70	ACT ATT TCA AAC AAT CTT TTT TTC AAC CAT CAT AAA GTG ATG TTG TTA Thr Ile Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu 190 195 200	731
	GGG CAT GAT GAT GCA TAT AGT GAT GAC AAA TCC ATG AAG GTG ACA GTG Gly His Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val 205 210 215	779
	GCG TTC AAT CAA TTT GGA CCT AAC TGT GGA CAA AGA ATG CCC AGG GCA Ala Phe Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala 220 225 230	827
	CGA TAT GGA CTT GTA CAT GTT GCA AAC AAT AAT TAT GAC CCA TGG ACT Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr 235 240 245	875

70

Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn Glu Ser
 125 130 135
 5 Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu Thr Leu
 140 145 150
 Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser Asn Ser
 160 165 170
 10 Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val Thr Ile
 175 180 185
 Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu Gly His
 190 195 200
 15 Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe
 205 210 215
 20 Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala Arg Tyr
 220 225 230 235
 Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr Ile Tyr
 240 245 250
 25 Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly Asn Ser
 255 260 265
 Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile Arg Ile
 270 275 280
 30 Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp Gln Ser Thr
 285 290 295
 35 Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr
 300 305 310 315
 Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu Asn
 320 325 330
 40 Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu Thr Cys
 335 340 345
 45 Ser Leu Ser Lys Arg Cys
 350

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAYAAAYCCNA THGAYWS

17

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGAATTCAA YTGGGCNCAR AAYSG

25

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION: 15
(D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGCAGCCRT TYTCNACRTT RAA

23

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION: 6
(D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCATNCKRT TYTGNGCCCA

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTGCAGCKR TTYTGNGCCC AARTT

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGATTCCC CTTGCTTA

18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAATTCGA TAATCCCATATA GACAGC

26

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
10 ATGCCTATGT ACATTGC 17

(2) INFORMATION FOR SEQ ID NO:11:
15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
20 GCAATGTACA TAGGCAT 17

(2) INFORMATION FOR SEQ ID NO:12:
25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
35 TCCAATTCTT CTGATGGT 18

(2) INFORMATION FOR SEQ ID NO:13:
40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
45 TTTTGTCAAT TGAGGAGT 18

(2) INFORMATION FOR SEQ ID NO:14:
50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
60 CCTGCAGAAG CTTTCATCAAC AACGTTTAGA 30

(2) INFORMATION FOR SEQ ID NO:15:
65

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
70 TAGCAACTCC AGTCGAAGT 19

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAGCTCTCAT TTGGTGC

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TATGCAATTG GTGGGAGT

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptomeria japonica*

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "the amino acid at position
7 is Ser, Cys, Thr, or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp Asn Pro Ile Asp Ser Xaa Trp Arg Gly Asp Ser Asn Trp Ala Gln
 1 5 10 15

Asn Arg Met Lys
 20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptomeria japonica*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu Ala Phe Asn Val Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
GGGTCTAGAG GTACCGTCCG ATCGATCATT 30

10 (2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
20 GGGTCTAGAG GTACCGTCCG 20

(2) INFORMATION FOR SEQ ID NO:22:
(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
AATGATCGAT GCT 13

35 (2) INFORMATION FOR SEQ ID NO:23:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
45 GGAATTCTCT AGACTGCAGG T 21

(2) INFORMATION FOR SEQ ID NO:24:
(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
GGAATTCTCT AGACTGCAGG TTTTTTTTTT TTTT 35

(2) INFORMATION FOR SEQ ID NO:25:
60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: N-terminal

70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Juniperus sabinoides

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Asn Pro Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp Ser Asn Trp Ala Gln
1 5 10 15
Asn Arg Met Lys
20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala Val
1 5 10 15
Gly Phe Gly Ser
20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Ala Asp Cys Ala Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys
1 5 10 15
Gly Gly Asp Leu
20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

5 Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr Thr Val Thr Asn Ser
 1 5 10 15
 Asp Asp Asp Pro
 20

10 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

25 Tyr Thr Val Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly
 1 5 10 15
 Thr Leu Arg Tyr
 20

30 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

45 Val Asn Pro Ala Pro Gly Thr Leu Arg Tyr Gly Ala Thr Arg Asp Arg
 1 5 10 15
 Pro Leu Trp Ile
 20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

60 Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser Gly Asn Met
 1 5 10 15

65 Asn Ile Lys Leu
 20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Phe Ser Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile
 1 5 10 15
 Ala Gly Tyr Lys
 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Lys Met Pro Met Tyr Ile Ala Gly Tyr Lys Thr Phe Asp Gly Arg Gly
 1 5 10 15
 Ala Gln Val Tyr
 20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly Pro
 1 5 10 15
 Cys Val Phe Ile
 20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ile Gly Asn Gly Gly Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val
 1 5 10 15
 Ile Ile His Gly
 20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Lys Arg Val Ser Asn Val Ile Ile His Gly Leu Tyr Leu Tyr Gly Cys
1 5 10 15
Ser Thr Ser Val
20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Leu Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile
1 5 10 15
Asn Glu Ser Phe
20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Leu Gly Asn Val Leu Ile Asn Glu Ser Phe Gly Val Glu Pro Val His
1 5 10 15
Pro Gln Asp Gly
20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu Thr Leu Arg
1 5 10 15
Thr Ala Thr Asn
20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Asp Ala Leu Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn
 1 5 10 15
 Ser Phe Ser Asn
 20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ile Trp Ile Asp His Asn Ser Phe Ser Asn Ser Ser Asp Gly Leu Val
 1 5 10 15
 Asp Val Thr Leu
 20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val Thr
 1 5 10 15
 Ile Ser Asn Asn
 20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Thr Ser Thr Gly Val Thr Ile Ser Asn Asn Leu Phe Phe Asn His His
 1 5 10 15

5 Lys Val Met Leu
 20

(2) INFORMATION FOR SEQ ID NO:45:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

20 Leu Phe Phe Asn His His Lys Val Met Leu Leu Gly His Asp Asp Ala
 1 5 10 15

25 Tyr Ser Asp Asp
 20

(2) INFORMATION FOR SEQ ID NO:46:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

40 Leu Gly His Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr
 1 5 10 15

45 Val Ala Phe Asn
 20

(2) INFORMATION FOR SEQ ID NO:47:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

60 Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys
 1 5 10 15

65 Gly Gln Arg Met
 20

(2) INFORMATION FOR SEQ ID NO:48:

70 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly
1 5 10 15

10 Leu Val His Val
20

(2) INFORMATION FOR SEQ ID NO:49:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Pro Arg Ala Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp
1 5 10 15

30 Pro Trp Thr Ile
20

(2) INFORMATION FOR SEQ ID NO:50:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

45 Ala Asn Asn Asn Tyr Asp Pro Trp Thr Ile Tyr Ala Ile Gly Gly Ser
1 5 10 15

50 Ser Asn Pro Thr
20

(2) INFORMATION FOR SEQ ID NO:51:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

65 Tyr Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly Asn
1 5 10 15

Ser Phe Thr Ala
20

70 (2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Leu Ser Glu Gly Asn Ser Phe Thr Ala Pro Asn Glu Ser Tyr Lys
1 5 10 15
Lys Gln Val Thr
20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile Arg Ile Gly Cys Lys
1 5 10 15
Thr Ser Ser Ser
20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ile Arg Ile Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp
1 5 10 15
Gln Ser Thr Gln
20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Cys Ser Asn Trp Val Trp Gln Ser Thr Gln Asp Val Phe Tyr Asn Gly
1 5 10 15
Ala Tyr Phe Val
20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu
 1 5 10 15
 Gly Gly Asn Ile
 20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ser Ser Gly Lys Tyr Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala
 1 5 10 15
 Phe Asn Val Glu
 20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu Asn Gly Asn Ala Thr Pro
 1 5 10 15
 Gln Leu Thr Lys
 20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu Thr
 1 5 10 15

Cys Ser Leu Ser
 20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asn Ala Gly Val Leu Thr Cys Ser Leu Ser Lys Arg Cys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp Ser Asn Trp Ala Gln
 1 5 10 15

Asn Arg Met Lys Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala
 20 25 30

Asp Cys Ala Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly
 35 40 45

Asp Leu Tyr Thr Val Thr Asn Ser Asp Asp Asp Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser Gly Asn Met
 1 5 10 15

Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr Lys Thr Phe
 20 25 30

Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly Pro Cys Val
 35 40 45

Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly
 50 55 60

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Leu Gly Asn Val Leu Ile Asn Glu Ser Phe Gly Val Glu Pro Val His
 1 5 10 15
 Pro Gln Asp Gly Asp Ala Leu Thr Leu Arg Thr Ala Thr Asn Ile Trp
 20 25 30
 Ile Asp His Asn Ser Phe Ser Asn Ser Ser Asp Gly Leu Val Asp Val
 35 40 45
 Thr Leu
 50

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Phe Phe Asn His His Lys Val Met Leu Leu Gly His Asp Asp Ala
 1 5 10 15
 Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe
 20 25 30
 Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Leu Val
 35 40 45
 His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr Ile Tyr Ala Ile Gly
 50 55 60
 Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly Asn Ser Phe Thr Ala
 65 70 75 80
 Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr
 85 90

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Cys Ser Asn Trp Val Trp Gln Ser Thr Gln Asp Val Phe Tyr Asn Gly
 1 5 10 15
 5 Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly Asn Ile Tyr Thr
 20 25 30
 Lys Lys Glu Ala Phe Asn Val Glu Asn Gly Asn Ala Thr Pro Gln Leu
 35 40 45
 10 Thr Lys Asn Ala Gly Val Leu Thr Cys Ser Leu Ser Lys Arg Cys
 50 55 60

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp Ser Asn Trp Ala Gln
 1 5 10 15
 30 Asn Arg Met Lys Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala
 20 25 30
 Asp Cys Ala Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly
 35 40 45
 35 Asp Leu
 50

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Met Pro Met Tyr Ile Ala Gly Tyr Lys Thr Phe Asp Gln Arg Gly
 1 5 10 15
 55 Ala Gln Val Tyr Ile Gly Asn Gly Gly Pro Cys Val Phe Ile
 20 25 30

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asp Ala Leu Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn
 1 5 10 15
 Ser Phe Ser Asn Ser Ser Asp Gly Leu Val Asp Val Thr Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Leu Phe Phe Asn His His Lys Val Met Leu Leu Gly His Asp Asp Ala
 1 5 10 15
 Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe
 20 25 30
 Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Leu Val
 35 40 45
 His Val
 50

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

Cys Ser Asn Trp Val Trp Gln Ser Thr Gln Asp Val Phe Tyr Asn Gly
 1 5 10 15
 Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly Asn Ile Tyr Thr
 20 25 30
 Lys Lys Glu Ala Phe Asn Val Glu
 35 40

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Lys Met Pro Met Tyr Ile Ala Gly Tyr Lys Thr Phe Asp Gly Arg Gly
 1 5 10 15
 Ala Gln Val Tyr Ile Gly Asn Gly Gly Pro Cys Val Phe Ile
 20 25 30

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Pro Met Tyr Ile Ala Gly Tyr Lys Thr Phe Asp Gly Arg Gly Ala Gln
 1 5 10 15
 Val Tyr Ile Gly Asn Gly Gly Pro
 20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Tyr Ile Ala Gly Tyr Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr
 1 5 10 15
 Ile Gly Asn Gly Gly Pro
 20

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Lys Lys Tyr Ile Ala Gly Tyr Lys Thr Phe Asp Gly Arg Gly Ala Gln
 1 5 10 15
 Val Tyr Ile Gly Asn Gly Gly Pro
 20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asp	Ala	Leu	Thr	Leu	Arg	Thr	Ala	Thr	Asn	Ile	Trp	Ile	Asp	His	Asn
1				5					10					15	
Ser	Phe	Ser	Asn	Ser	Ser	Asp	Gly	Leu	Val	Asp	Val	Thr	Leu		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Arg	Thr	Ala	Thr	Asn	Ile	Trp	Ile	Asp	His	Asn	Ser	Phe	Ser	Asn	Ser
1				5					10					15	
Ser	Asp	Gly	Leu	Val	Asp										
			20												

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Lys	Arg	Thr	Ala	Thr	Asn	Ile	Trp	Ile	Asp	His	Asn	Ser	Phe	Ser	Asn
1				5					10					15	
Ser	Ser	Asp	Gly	Leu	Val	Asp	Lys								
			20												

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys
 1 5 10 15
 Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Leu Val His Val Ala Asn
 20 25 30
 Asn Asn Tyr Asp
 35

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys
 1 5 10 15
 Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Leu Val His Val
 20 25 30

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Ser
 1 5 10 15
 Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Leu Val His Val
 20 25 30

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys
 1 5 10 15

Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Leu Val
 20 25

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys
 1 5 10 15

Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Leu Val
 20 25

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys
 1 5 10 15

Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Ser
 1 5 10 15

Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Ser
 1 5 10 15
 Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Lys Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys
 1 5 10 15
 Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Pro Arg Ala Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp
 1 5 10 15
 Pro Trp Thr Ile Tyr Ala Ile Gly Gly Ser Ser Asn Pro Thr
 20 25 30

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Arg Ala Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro
 1 5 10 15

Trp Thr Ile Tyr Ala Ile Gly Gly Ser Ser Asn Pro
 20 25

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Arg Ala Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro
 1 5 10 15

Trp Thr Ile Tyr Ala Ile Gly Gly Ser Ser
 20 25

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu
 1 5 10 15

Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu
 20 25 30

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly Asn Ile
 1 5 10 15

Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly Asn Ile
 1 5 10 15

Tyr Thr Lys Lys Glu Ala Phe Asn
 20

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Lys Lys Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly
 1 5 10 15

Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn
 20 25

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 26..1126

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 89..1126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AAATTCTATA TTCTGAACCC TAAAA ATG GCT TCC CCA TGC TTA ATA GCA GTC 52
 Met Ala Ser Pro Cys Leu Ile Ala Val
 -21 -20 -15
 CTT GTT TTC CTT TGT GCA ATT GTA TCT TGT TAC TCT GAT AAT CCC ATC 100
 Leu Val Phe Leu Cys Ala Ile Val Ser Cys Tyr Ser Asp Asn Pro Ile
 -10 -5 1

	GAC	AGC	TGC	TGG	AGA	GGA	GAT	TCG	AAC	TGG	GAT	CAA	AAC	AGA	ATG	AAG	148
	Asp	Ser	Cys	Trp	Arg	Gly	Asp	Ser	Asn	Trp	Asp	Gln	Asn	Arg	Met	Lys	
	5					10					15					20	
5	CTC	GCA	GAC	TGT	GCT	GTG	GGA	TTT	GGA	AGC	TCC	ACC	ATG	GGA	GGC	AAA	196
	Leu	Ala	Asp	Cys	Ala	Val	Gly	Phe	Gly	Ser	Ser	Thr	Met	Gly	Gly	Lys	
					25					30					35		
10	GGA	GGA	GAT	TTT	TAC	ACC	GTC	ACA	AGC	ACA	GAT	GAT	AAT	CCT	GTG	AAT	244
	Gly	Gly	Asp	Phe	Tyr	Thr	Val	Thr	Ser	Thr	Asp	Asp	Asn	Pro	Val	Asn	
				40					45					50			
15	CCT	ACA	CCA	GGA	ACT	TTG	CGC	TAT	GGA	GCA	ACA	AGA	GAA	AAA	GCA	CTT	292
	Pro	Thr	Pro	Gly	Thr	Leu	Arg	Tyr	Gly	Ala	Thr	Arg	Glu	Lys	Ala	Leu	
			55					60					65				
20	TGG	ATC	ATT	TTC	TCT	CAG	AAT	ATG	AAT	ATA	AAG	CTC	AAG	ATG	CCT	TTG	340
	Trp	Ile	Ile	Phe	Ser	Gln	Asn	Met	Asn	Ile	Lys	Leu	Lys	Met	Pro	Leu	
		70					75					80					
25	TAT	GTT	GCT	GGA	CAT	AAG	ACT	ATT	GAC	GGC	AGG	GGA	GCA	GAT	GTT	CAT	388
	Tyr	Val	Ala	Gly	His	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Asp	Val	His	
	85					90				95					100		
30	CTT	GGC	AAC	GGC	GGT	CCC	TGT	CTG	TTT	ATG	AGG	AAA	GTG	AGC	CAT	GTT	436
	Leu	Gly	Asn	Gly	Gly	Pro	Cys	Leu	Phe	Met	Arg	Lys	Val	Ser	His	Val	
				105						110					115		
35	ATT	CTC	CAT	AGT	TTG	CAT	ATA	CAC	GGT	TGT	AAT	ACG	AGT	GTT	TTG	GGG	484
	Ile	Leu	His	Ser	Leu	His	Ile	His	Gly	Cys	Asn	Thr	Ser	Val	Leu	Gly	
				120					125					130			
40	GAT	GTT	TTG	GTA	AGT	GAG	TCT	ATT	GGG	GTC	GAG	CCT	GTT	CAT	GCT	CAG	532
	Asp	Val	Leu	Val	Ser	Glu	Ser	Ile	Gly	Val	Glu	Pro	Val	His	Ala	Gln	
			135					140					145				
45	GAT	GGG	GAC	GCC	ATT	ACT	ATG	CGC	CAT	GTT	ACA	AAT	GCT	TGG	ATT	GAT	580
	Asp	Gly	Asp	Ala	Ile	Thr	Met	Arg	His	Val	Thr	Asn	Ala	Trp	Ile	Asp	
		150					155					160					
50	CAT	AAT	TCT	CTC	TCC	GAT	TGT	TCT	GAT	GGT	CTT	ATC	GAT	GTT	ACG	CTT	628
	His	Asn	Ser	Leu	Ser	Asp	Cys	Ser	Asp	Gly	Leu	Ile	Asp	Val	Thr	Leu	
	165					170				175						180	
55	GGC	TCC	ACT	GGA	ATT	ACT	ATC	TCC	AAC	AAT	CAC	TTC	TTC	AAC	CAT	CAT	676
	Gly	Ser	Thr	Gly	Ile	Thr	Ile	Ser	Asn	Asn	His	Phe	Phe	Asn	His	His	
				185						190					195		
60	AAA	GTG	ATG	TTA	TTA	GGA	CAT	GAT	GAT	ACA	TAT	GAC	GAT	GAC	AAA	TCT	724
	Lys	Val	Met	Leu	Leu	Gly	His	Asp	Asp	Thr	Tyr	Asp	Asp	Asp	Lys	Ser	
				200				205					210				
65	ATG	AAA	GTG	ACA	GTG	GCG	TTC	AAT	CAA	TTT	GGA	CCT	AAT	GCT	GGG	CAA	772
	Met	Lys	Val	Thr	Val	Ala	Phe	Asn	Gln	Phe	Gly	Pro	Asn	Ala	Gly	Gln	
			215					220					225				
70	AGA	ATG	CCA	AGG	GCA	CGA	TAT	GGA	CTT	GTA	CAT	GTT	GCA	AAC	AAT	AAT	820
	Arg	Met	Pro	Arg	Ala	Arg	Tyr	Gly	Leu	Val	His	Val	Ala	Asn	Asn	Asn	
		230					235					240					
75	TAT	GAT	CCA	TGG	AAT	ATA	TAT	GCT	ATT	GGT	GGG	AGT	TCA	AAT	CCA	ACC	868
	Tyr	Asp	Pro	Trp	Asn	Ile	Tyr	Ala	Ile	Gly	Gly	Ser	Ser	Asn	Pro	Thr	
	245					250				255						260	

	ATT CTG AGT GAA GGG AAT AGT TTC ACT GCC CCA AGT GAG AGT TAC AAG	916
	Ile Leu Ser Glu Gly Asn Ser Phe Thr Ala Pro Ser Glu Ser Tyr Lys	
	265 270 275	
5	AAG CAA GTA ACA AAG CGT ATA GGG TGT GAA TCA CCA TCA GCT TGT GCG	964
	Lys Gln Val Thr Lys Arg Ile Gly Cys Glu Ser Pro Ser Ala Cys Ala	
	280 285 290	
10	AAC TGG GTG TGG AGA TCT ACA CGA GAT GCT TTT ATT AAT GGA GCT TAT	1012
	Asn Trp Val Trp Arg Ser Thr Arg Asp Ala Phe Ile Asn Gly Ala Tyr	
	295 300 305	
15	TTT GTA TCA TCG GGG AAA ACT GAA GAG ACC AAT ATA TAC AAT AGT AAT	1060
	Phe Val Ser Ser Gly Lys Thr Glu Glu Thr Asn Ile Tyr Asn Ser Asn	
	310 315 320	
20	GAA GCT TTC AAA GTT GAG AAT GGG AAT GCA GCT CCT CAA TTA ACC AAA	1108
	Glu Ala Phe Lys Val Glu Asn Gly Asn Ala Ala Pro Gln Leu Thr Lys	
	325 330 335 340	
	AAT GCT GGA GTT GTA ACC TAAGCTCTCT CTAAATCTTG CTTATGAAAC	1156
	Asn Ala Gly Val Thr	
	345	
25	GAAAAAATAT ATAG	1170
	(2) INFORMATION FOR SEQ ID NO:95:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 367 amino acids	
	(B) TYPE: amino acid	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
40	Met Ala Ser Pro Cys Leu Ile Ala Val Leu Val Phe Leu Cys Ala Ile	
	-21 -20 -15 -10	
	Val Ser Cys Tyr Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp	
	-5 1 5 10	
45	Ser Asn Trp Asp Gln Asn Arg Met Lys Leu Ala Asp Cys Ala Val Gly	
	15 20 25	
	Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Phe Tyr Thr Val	
	30 35 40	
50	Thr Ser Thr Asp Asp Asn Pro Val Asn Pro Thr Pro Gly Thr Leu Arg	
	45 50 55	
55	Tyr Gly Ala Thr Arg Glu Lys Ala Leu Trp Ile Ile Phe Ser Gln Asn	
	60 65 70 75	
	Met Asn Ile Lys Leu Lys Met Pro Leu Tyr Val Ala Gly His Lys Thr	
	80 85 90	
60	Ile Asp Gly Arg Gly Ala Asp Val His Leu Gly Asn Gly Gly Pro Cys	
	95 100 105	
	Leu Phe Met Arg Lys Val Ser His Val Ile Leu His Ser Leu His Ile	
	110 115 120	
65		

5 His Gly Cys Asn Thr Ser Val Leu Gly Asp Val Leu Val Ser Glu Ser
 125 130 135
 Ile Gly Val Glu Pro Val His Ala Gln Asp Gly Asp Ala Ile Thr Met
 140 145 150 155
 Arg His Val Thr Asn Ala Trp Ile Asp His Asn Ser Leu Ser Asp Cys
 160 165 170
 10 Ser Asp Gly Leu Ile Asp Val Thr Leu Gly Ser Thr Gly Ile Thr Ile
 175 180 185
 Ser Asn Asn His Phe Phe Asn His His Lys Val Met Leu Leu Gly His
 190 195 200
 15 Asp Asp Thr Tyr Asp Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe
 205 210 215
 Asn Gln Phe Gly Pro Asn Ala Gly Gln Arg Met Pro Arg Ala Arg Tyr
 220 225 230 235
 20 Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Asn Ile Tyr
 240 245 250
 25 Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly Asn Ser
 255 260 265
 Phe Thr Ala Pro Ser Glu Ser Tyr Lys Lys Gln Val Thr Lys Arg Ile
 270 275 280
 30 Gly Cys Glu Ser Pro Ser Ala Cys Ala Asn Trp Val Trp Arg Ser Thr
 285 290 295
 Arg Asp Ala Phe Ile Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Thr
 300 305 310 315
 35 Glu Glu Thr Asn Ile Tyr Asn Ser Asn Glu Ala Phe Lys Val Glu Asn
 320 325 330
 40 Gly Asn Ala Ala Pro Gln Leu Thr Lys Asn Ala Gly Val Val Thr
 335 340 345

(2) INFORMATION FOR SEQ ID NO:96:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 36..1145

55 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 99..1145

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

65 CGGTATAGAT AGATTCTATA TTCTGAGCCC TAAAA ATG GCT TCC CCA TGC TTA
 Met Ala Ser Pro Cys Leu
 -21 -20

53

	ATA	GCA	TTC	CTT	GTT	TTC	CTT	TGT	GCA	ATT	GTA	TCT	TGT	TGC	TCT	GAT	101
	Ile	Ala	Phe	Leu	Val	Phe	Leu	Cys	Ala	Ile	Val	Ser	Cys	Cys	Ser	Asp	
	-15					-10					-5					1	
5	AAT	CCC	ATA	GAC	AGC	TGC	TGG	AGA	GGA	GAT	TCG	AAC	TGG	GGT	CAA	AAC	149
	Asn	Pro	Ile	Asp	Ser	Cys	Trp	Arg	Gly	Asp	Ser	Asn	Trp	Gly	Gln	Asn	
				5					10					15			
10	AGA	ATG	AAG	CTC	GCA	GAT	TGC	GCT	GTG	GGA	TTT	GGA	AGC	TCC	ACC	ATG	197
	Arg	Met	Lys	Leu	Ala	Asp	Cys	Ala	Val	Gly	Phe	Gly	Ser	Ser	Thr	Met	
			20					25					30				
15	GGA	GGC	AAA	GGA	GGA	GAT	TTT	TAC	ACC	GTC	ACA	AGC	GCA	GAT	GAT	AAT	245
	Gly	Gly	Lys	Gly	Gly	Asp	Phe	Tyr	Thr	Val	Thr	Ser	Ala	Asp	Asp	Asn	
		35					40					45					
20	CCT	GTG	AAT	CCT	ACA	CCA	GGA	ACT	TTG	CGC	TAT	GGA	GCA	ACA	AGA	GAA	293
	Pro	Val	Asn	Pro	Thr	Pro	Gly	Thr	Leu	Arg	Tyr	Gly	Ala	Thr	Arg	Glu	
	50					55					60					65	
	AAA	GCA	CTT	TGG	ATC	ATT	TTC	TCT	CAG	AAT	ATG	AAT	ATA	AAG	CTC	AAG	341
	Lys	Ala	Leu	Trp	Ile	Ile	Phe	Ser	Gln	Asn	Met	Asn	Ile	Lys	Leu	Lys	
					70				75						80		
25	ATG	CCT	TTG	TAT	GTT	GCT	GGA	CAT	AAG	ACT	ATT	GAC	GGC	AGG	GGA	GCA	389
	Met	Pro	Leu	Tyr	Val	Ala	Gly	His	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	
				85					90					95			
30	GAT	GTT	CAT	CTT	GGC	AAC	GGC	GGT	CCC	TGT	CTG	TTT	ATG	AGG	AAA	GTG	437
	Asp	Val	His	Leu	Gly	Asn	Gly	Gly	Pro	Cys	Leu	Phe	Met	Arg	Lys	Val	
			100					105					110				
35	AGC	CAT	GTT	ATT	CTC	CAT	GGT	TTG	CAT	ATA	CAC	GGT	TGT	AAT	ACT	AGT	485
	Ser	His	Val	Ile	Leu	His	Gly	Leu	His	Ile	His	Gly	Cys	Asn	Thr	Ser	
		115					120					125					
40	GTT	TTG	GGG	GAT	GTT	TTG	GTA	AGT	GAG	TCT	ATT	GGG	GTG	GTG	CCT	GTA	533
	Val	Leu	Gly	Asp	Val	Leu	Val	Ser	Glu	Ser	Ile	Gly	Val	Val	Pro	Val	
	130					135					140					145	
	CAC	CCC	CAG	GAC	GGA	GAT	GCG	TTT	ACT	GTG	AGG	ACC	TCT	GAA	CAT	ATT	581
	His	Pro	Gln	Asp	Gly	Asp	Ala	Phe	Thr	Val	Arg	Thr	Ser	Glu	His	Ile	
					150					155					160		
45	TGG	GTC	GAC	CAT	AAT	ACT	CTC	TCC	AAT	GGC	ACC	GAC	GGC	CTC	GTC	GAC	629
	Trp	Val	Asp	His	Asn	Thr	Leu	Ser	Asn	Gly	Thr	Asp	Gly	Leu	Val	Asp	
				165				170						175			
50	GTT	ACT	CTT	GCT	TCC	ACT	GCT	GTT	ACT	ATT	TCC	AAT	AAC	CAC	TTC	TTC	677
	Val	Thr	Leu	Ala	Ser	Thr	Ala	Val	Thr	Ile	Ser	Asn	Asn	His	Phe	Phe	
			180					185					190				
55	GAC	CAT	GAT	GAA	GTG	ATG	TTG	TTA	GGA	CAT	AGT	GAT	TCA	TTC	TCA	GAT	725
	Asp	His	Asp	Glu	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Ser	Phe	Ser	Asp	
		195					200					205					
60	GAT	AAA	GTG	ATG	AAA	GTC	ACA	GTT	GCA	TTT	AAC	CAC	TTT	GGA	CCT	AAT	773
	Asp	Lys	Val	Met	Lys	Val	Thr	Val	Ala	Phe	Asn	His	Phe	Gly	Pro	Asn	
	210					215					220					225	
	TGT	GTG	CAA	CGA	TTG	CCA	AGG	GCT	AGA	TAT	GGA	CAC	TTT	CAT	GTT	GTT	821
	Cys	Val	Gln	Arg	Leu	Pro	Arg	Ala	Arg	Tyr	Gly	His	Phe	His	Val	Val	
					230					235					240		

	AAT	AAT	AAT	TAT	GAG	CCA	TGG	GGA	AAA	TAT	GCC	ATT	GGA	GGA	AGT	TCT	869
	Asn	Asn	Asn	Tyr	Glu	Pro	Trp	Gly	Lys	Tyr	Ala	Ile	Gly	Gly	Ser	Ser	
				245					250						255		
5	GAT	CCA	ACA	ATT	ATA	AGT	GAA	GGG	AAT	AGA	TTT	CTT	GCA	CCA	AAT	GAA	917
	Asp	Pro	Thr	Ile	Ile	Ser	Glu	Gly	Asn	Arg	Phe	Leu	Ala	Pro	Asn	Glu	
			260					265					270				
10	TCT	TAT	AAA	AAG	GAG	GTG	ACA	ATA	CGT	GTA	GGT	TGT	AAA	TCT	ACA	AGT	965
	Ser	Tyr	Lys	Lys	Glu	Val	Thr	Ile	Arg	Val	Gly	Cys	Lys	Ser	Thr	Ser	
			275				280					285					
15	TGT	GAT	GCA	TGG	GAG	TGG	AGA	TCA	AAA	GAT	GAT	GCC	TTC	CTT	AAT	GGT	1013
	Cys	Asp	Ala	Trp	Glu	Trp	Arg	Ser	Lys	Asp	Asp	Ala	Phe	Leu	Asn	Gly	
	290					295				300						305	
20	GCC	TAT	TTT	GTA	CAA	TCA	GGC	AAG	GGG	TAT	AAT	GGT	GGA	GAG	GCA	TTC	1061
	Ala	Tyr	Phe	Val	Gln	Ser	Gly	Lys	Gly	Tyr	Asn	Gly	Gly	Glu	Ala	Phe	
				310						315					320		
25	AAG	GTT	GAA	AGT	GCA	AAT	GAG	GTG	CCA	ACA	TTG	ACT	AAA	CAT	GCT	GGA	1109
	Lys	Val	Glu	Ser	Ala	Asn	Glu	Val	Pro	Thr	Leu	Thr	Lys	His	Ala	Gly	
				325				330						335			
30	GCA	TTA	AAA	TGT	ATA	CCT	ACC	AAA	CAA	TGT	GTG	ATA	TGAAAAGTCA				1155
	Ala	Leu	Lys	Cys	Ile	Pro	Thr	Lys	Gln	Cys	Val	Ile					
			340					345									
35	ATCGATATAA	TAATGTGTTA	TTTGTAATAT	TTCAGCTTTG	AATATGTATA	GAAAAAGAAT											1215
40	TTCAACAAAA	TGACACTATT	ATATAAATAA	ATTCTTAGTT	TATTAGTTGG	TATTAAAAAA											1275
	AAA																1278

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Met	Ala	Ser	Pro	Cys	Leu	Ile	Ala	Phe	Leu	Val	Phe	Leu	Cys	Ala	Ile
-21	-20					-15					-10				
Val	Ser	Cys	Cys	Ser	Asp	Asn	Pro	Ile	Asp	Ser	Cys	Trp	Arg	Gly	Asp
-5					1				5					10	
Ser	Asn	Trp	Gly	Gln	Asn	Arg	Met	Lys	Leu	Ala	Asp	Cys	Ala	Val	Gly
			15					20					25		
Phe	Gly	Ser	Ser	Thr	Met	Gly	Gly	Lys	Gly	Gly	Asp	Phe	Tyr	Thr	Val
	30					35					40				
Thr	Ser	Ala	Asp	Asp	Asn	Pro	Val	Asn	Pro	Thr	Pro	Gly	Thr	Leu	Arg
	45					50					55				
Tyr	Gly	Ala	Thr	Arg	Glu	Lys	Ala	Leu	Trp	Ile	Ile	Phe	Ser	Gln	Asn
60					65				70					75	
Met	Asn	Ile	Lys	Leu	Lys	Met	Pro	Leu	Tyr	Val	Ala	Gly	His	Lys	Thr
				80					85					90	

Ile Asp Gly Arg Gly Ala Asp Val His Leu Gly Asn Gly Gly Pro Cys
 95 100 105
 5 Leu Phe Met Arg Lys Val Ser His Val Ile Leu His Gly Leu His Ile
 110 115 120
 His Gly Cys Asn Thr Ser Val Leu Gly Asp Val Leu Val Ser Glu Ser
 125 130 135
 10 Ile Gly Val Val Pro Val His Pro Gln Asp Gly Asp Ala Phe Thr Val
 140 145 150 155
 Arg Thr Ser Glu His Ile Trp Val Asp His Asn Thr Leu Ser Asn Gly
 160 165 170
 15 Thr Asp Gly Leu Val Asp Val Thr Leu Ala Ser Thr Ala Val Thr Ile
 175 180 185
 Ser Asn Asn His Phe Phe Asp His Asp Glu Val Met Leu Leu Gly His
 190 195 200
 Ser Asp Ser Phe Ser Asp Asp Lys Val Met Lys Val Thr Val Ala Phe
 205 210 215
 25 Asn His Phe Gly Pro Asn Cys Val Gln Arg Leu Pro Arg Ala Arg Tyr
 220 225 230 235
 Gly His Phe His Val Val Asn Asn Asn Tyr Glu Pro Trp Gly Lys Tyr
 240 245 250
 30 Ala Ile Gly Gly Ser Ser Asp Pro Thr Ile Ile Ser Glu Gly Asn Arg
 255 260 265
 Phe Leu Ala Pro Asn Glu Ser Tyr Lys Lys Glu Val Thr Ile Arg Val
 270 275 280
 35 Gly Cys Lys Ser Thr Ser Cys Asp Ala Trp Glu Trp Arg Ser Lys Asp
 285 290 295
 40 Asp Ala Phe Leu Asn Gly Ala Tyr Phe Val Gln Ser Gly Lys Gly Tyr
 300 305 310 315
 Asn Gly Gly Glu Ala Phe Lys Val Glu Ser Ala Asn Glu Val Pro Thr
 320 325 330
 45 Leu Thr Lys His Ala Gly Ala Leu Lys Cys Ile Pro Thr Lys Gln Cys
 335 340 345
 Val Ile

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGGCTCGAGC TGCAGTTTTT TTTTTTTTTT TTV

33

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
5 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
CATAAAATGG CTTCCCCA 18

(2) INFORMATION FOR SEQ ID NO:100:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:
CGGGAATTCT AGATGTGCAA TTGTATCTTG TTA 33

(2) INFORMATION FOR SEQ ID NO:101:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
CGGGAATTCT AGATGTGCAA TAGTATCTTG TTG 33

(2) INFORMATION FOR SEQ ID NO:102:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
GGAATTCTCT AGACTGCAGG T 21

(2) INFORMATION FOR SEQ ID NO:103:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGAATTCTCT AGACTGCAGG TTTTTTTTTT TTTT

35

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GGCCTGCAGY YARCANCKKT TNSMNARNRW RCA

33

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CCRCTRAADA TDATA

17

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCRTCCCCRT CYTGNGGRTG

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTCCAYGGRT CRTARTTRTT

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GCCCTGCAGT CCCCRTCYTG NGGRTGNAC

29

10 (2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GCTCCACCAT GGDAGGCA

18

(2) INFORMATION FOR SEQ ID NO:110:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

35 CAYCCNCARG AYGGGGAYGC

20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

50 CGGGAATTCC CTCARGAYGG GGAYGCNY

28

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TAGGACATGA TGATACAT

18

65

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAGATCTACA CGAGATGC

18

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

RAAWCTATTC CCTTCACT

18

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TAGGACATAG TGATTCAT

18

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CCGGGATCCT TACAAATAAC ACATTAT

27

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

A2
 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:
 CCGGGATCCT TACAAATAAC ACATTAT

27

(2) INFORMATION FOR SEQ ID NO:117:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:
 CCCGAATTCA TGGCTTCCCC ATGCTTA

27

(2) INFORMATION FOR SEQ ID NO:118:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:
 CCGGGATCCC GTTTCATAAG CAAGATT

27

(2) INFORMATION FOR SEQ ID NO:119:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
 Asp Glu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser
 1 5 10 15
 Asn Ser Ser Asp Asp
 20

(2) INFORMATION FOR SEQ ID NO:120:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
 Asp Glu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser
 1 5 10 15
 Asn Ser Ser Asp Gly Leu Ala Asp
 20

(2) INFORMATION FOR SEQ ID NO:121:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

5 CCCGAATTCA TGGCTTCCCC ATGCTTA

27

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

20 CCGGGATCCC GTTTCATAAG CAAGATT

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

35 Asp Glu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser
1 5 10 15
Asn Ser Ser Asp Asp
20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

55 Asp Glu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser
1 5 10 15
Asn Ser Ser Asp Gly Leu Ala Asp
20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp Glu Lys Ser Met Lys Ala Thr Val Ala Phe Asn Gln Phe Gly Pro
1 5 10 15

Asn Asp Glu

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Asp Glu Lys Ser Met Lys Val Thr Ala Ala Phe Asn Gln Phe Gly Pro
1 5 10 15

Asn Asp Glu

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asp Glu Glu Lys Ser Met Lys Ala Thr Val Ala Phe Asn Glu Phe Gly
1 5 10 15

Pro Asn Asp Glu Glu
20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Glu Glu Lys Ser Met Lys Val Thr Val Ala Ala Asn Gln Phe Gly
1 5 10 15

Pro Asn Asp Glu Glu
20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Asp Glu Glu Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Ala Gly
1 5 10 15

Pro Asn Asp Glu Glu
20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp Glu Lys Ser Met Lys Ala Thr Ala Ala Phe Asn Gln Phe Gly Pro
1 5 10 15

Asn Asp Glu

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Asp Glu Glu Lys Ser Met Lys Ala Thr Ala Ala Phe Asn Gln Phe Gly
1 5 10 15

Pro Asn Asp Glu Glu
20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe
1 5 10 15

Asn Gln Phe Gly Asp Glu
20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp Lys Glu Pro Arg Ala Arg Tyr Gly Leu Val His Val Ala Asn Asn
1 5 10 15

Asn Tyr Asp Pro Trp Thr Ile Glu Glu Glu
20 25

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Glu Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly
1 5 10 15

Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Ala Glu
20 25

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Asp Glu Glu Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly
 1 5 10 15

5 Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:132:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Asp Glu Glu Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly
 1 5 10 15

25 Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:133:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1726 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

40 (A) NAME/KEY: CDS
 (B) LOCATION: 42..1586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

45 TGAGTTCGAG ACAAGTATAG AAAGAATTTT CTTTATTAA A ATG GCC ATG AAA 53
 Met Ala Met Lys
 1

50 TTA ATT GCT CCA ATG GCC TTT CTG GCC ATG CAA TTG ATT ATA ATG GCG 101
 Leu Ile Ala Pro Met Ala Phe Leu Ala Met Gln Leu Ile Ile Met Ala
 5 10 15 20

55 GCA GCA GAA GAT CAA TCT GCC CAA ATT ATG TTG GAC AGT GTT GTC GAA 149
 Ala Ala Glu Asp Gln Ser Ala Gln Ile Met Leu Asp Ser Val Val Glu
 25 30 35

60 AAA TAT CTT AGA TCG AAT CGG AGT TTA AGA AAA GTT GAG CAT TCT CGT 197
 Lys Tyr Leu Arg Ser Asn Arg Ser Leu Arg Lys Val Glu His Ser Arg
 40 45 50

CAT GAT GCT ATC AAC ATC TTC AAT GTG GAA AAG TAT GGC GCA GTA GGC 245
 His Asp Ala Ile Asn Ile Phe Asn Val Glu Lys Tyr Gly Ala Val Gly
 55 60 65

	GAT	GGA	AAG	CAT	GAT	TGC	ACT	GAG	GCA	TTT	TCA	ACA	GCA	TGG	CAA	GCT	293
	Asp	Gly	Lys	His	Asp	Cys	Thr	Glu	Ala	Phe	Ser	Thr	Ala	Trp	Gln	Ala	
		70					75					80					
5	GCA	TGC	AAA	AAC	CCA	TCA	GCA	ATG	TTG	CTT	GTG	CCA	GGC	AGC	AAG	AAA	341
	Ala	Cys	Lys	Asn	Pro	Ser	Ala	Met	Leu	Leu	Val	Pro	Gly	Ser	Lys	Lys	
		85				90					95					100	
10	TTT	GTT	GTA	AAC	AAT	CTG	TTC	TTC	AAT	GGG	CCA	TGT	CAA	CCT	CAC	TTT	389
	Phe	Val	Val	Asn	Asn	Leu	Phe	Phe	Asn	Gly	Pro	Cys	Gln	Pro	His	Phe	
					105					110					115		
15	ACT	TTT	AAG	GTA	GAT	GGG	ATA	ATA	GCT	GCG	TAC	CAA	AAT	CCA	GCG	AGC	437
	Thr	Phe	Lys	Val	Asp	Gly	Ile	Ile	Ala	Ala	Tyr	Gln	Asn	Pro	Ala	Ser	
				120					125					130			
20	TGG	AAG	AAT	AAT	AGA	ATA	TGG	TTG	CAG	TTT	GCT	AAA	CTT	ACA	GGT	TTT	485
	Trp	Lys	Asn	Asn	Arg	Ile	Trp	Leu	Gln	Phe	Ala	Lys	Leu	Thr	Gly	Phe	
			135				140						145				
25	ACT	CTA	ATG	GGT	AAA	GGT	GTA	ATT	GAT	GGG	CAA	GGA	AAA	CAA	TGG	TGG	533
	Thr	Leu	Met	Gly	Lys	Gly	Val	Ile	Asp	Gly	Gln	Gly	Lys	Gln	Trp	Trp	
		150					155					160					
30	GCT	GGC	CAA	TGT	AAA	TGG	GTC	AAT	GGA	CGA	GAA	ATT	TGC	AAC	GAT	CGT	581
	Ala	Gly	Gln	Cys	Lys	Trp	Val	Asn	Gly	Arg	Glu	Ile	Cys	Asn	Asp	Arg	
		165				170					175					180	
35	GAT	AGA	CCA	ACA	GCC	ATT	AAA	TTC	GAT	TTT	TCC	ACG	GGT	CTG	ATA	ATC	629
	Asp	Arg	Pro	Thr	Ala	Ile	Lys	Phe	Asp	Phe	Ser	Thr	Gly	Leu	Ile	Ile	
					185						190				195		
40	CAA	GGA	CTG	AAA	CTA	ATG	AAC	AGT	CCC	GAA	TTT	CAT	TTA	GTT	TTT	GGG	677
	Gln	Gly	Leu	Lys	Leu	Met	Asn	Ser	Pro	Glu	Phe	His	Leu	Val	Phe	Gly	
				200					205					210			
45	AAT	TGT	GAG	GGA	GTA	AAA	ATC	ATC	GGC	ATT	AGT	ATT	ACG	GCA	CCG	AGA	725
	Asn	Cys	Glu	Gly	Val	Lys	Ile	Ile	Gly	Ile	Ser	Ile	Thr	Ala	Pro	Arg	
			215					220					225				
50	GAC	AGT	CCT	AAC	ACT	GAT	GGA	ATT	GAT	ATC	TTT	GCA	TCT	AAA	AAC	TTT	773
	Asp	Ser	Pro	Asn	Thr	Asp	Gly	Ile	Asp	Ile	Phe	Ala	Ser	Lys	Asn	Phe	
		230					235					240					
55	CAC	TTA	CAA	AAG	AAC	ACG	ATA	GGA	ACA	GGG	GAT	GAC	TGC	GTC	GCT	ATA	821
	His	Leu	Gln	Lys	Asn	Thr	Ile	Gly	Thr	Gly	Asp	Asp	Cys	Val	Ala	Ile	
		245				250					255					260	
60	GGC	ACA	GGG	TCT	TCT	AAT	ATT	GTG	ATT	GAG	GAT	CTG	ATT	TGC	GGT	CCA	869
	Gly	Thr	Gly	Ser	Ser	Asn	Ile	Val	Ile	Glu	Asp	Leu	Ile	Cys	Gly	Pro	
					265					270					275		
65	GGC	CAT	GGA	ATA	AGT	ATA	GGA	AGT	CTT	GGG	AGG	GAA	AAC	TCT	AGA	GCA	917
	Gly	His	Gly	Ile	Ser	Ile	Gly	Ser	Leu	Gly	Arg	Glu	Asn	Ser	Arg	Ala	
				280					285					290			
70	GAG	GTT	TCA	TAC	GTG	CAC	GTA	AAT	GGG	GCT	AAA	TTC	ATA	GAC	ACA	CAA	965
	Glu	Val	Ser	Tyr	Val	His	Val	Asn	Gly	Ala	Lys	Phe	Ile	Asp	Thr	Gln	
			295					300					305				
75	AAT	GGA	TTA	AGA	ATC	AAA	ACA	TGG	CAG	GGT	GGT	TCA	GGC	ATG	GCA	AGC	1013
	Asn	Gly	Leu	Arg	Ile	Lys	Thr	Trp	Gln	Gly	Gly	Ser	Gly	Met	Ala	Ser	
		310					315					320					

	CAT ATA ATT TAT GAG AAT GTT GAA ATG ATA AAT TCG GAG AAC CCC ATA	1061
	His Ile Ile Tyr Glu Asn Val Glu Met Ile Asn Ser Glu Asn Pro Ile	
	325 330 335 340	
5	TTA ATA AAT CAA TTC TAC TGC ACT TCA GCT TCT GCT TGC CAA AAC CAG	1109
	Leu Ile Asn Gln Phe Tyr Cys Thr Ser Ala Ser Ala Cys Gln Asn Gln	
	345 350 355	
10	AGG TCT GCG GTT CAA ATC CAA GAT GTG ACA TAC AAG AAC ATA CGT GGG	1157
	Arg Ser Ala Val Gln Ile Gln Asp Val Thr Tyr Lys Asn Ile Arg Gly	
	360 365 370	
15	ACA TCA GCA ACA GCA GCA GCA ATT CAA CTT AAG TGC AGT GAC AGT ATG	1205
	Thr Ser Ala Thr Ala Ala Ala Ile Gln Leu Lys Cys Ser Asp Ser Met	
	375 380 385	
20	CCC TGC AAA GAT ATA AAG CTA AGT GAT ATA TCT TTG AAG CTT ACC TCA	1253
	Pro Cys Lys Asp Ile Lys Leu Ser Asp Ile Ser Leu Lys Leu Thr Ser	
	390 395 400	
25	GGG AAA ATT GCT TCC TGC CTT AAT GAT AAT GCA AAT GGA TAT TTC AGT	1301
	Gly Lys Ile Ala Ser Cys Leu Asn Asp Asn Ala Asn Gly Tyr Phe Ser	
	405 410 415 420	
30	GGA CAC GTC ATC CCT GCA TGC AAG AAT TTA AGT CCA AGT GCT AAG CGA	1349
	Gly His Val Ile Pro Ala Cys Lys Asn Leu Ser Pro Ser Ala Lys Arg	
	425 430 435	
35	AAA GAA TCT AAA TCC CAT AAA CAC CCA AAA ACT GTA ATG GTT GAA AAT	1397
	Lys Glu Ser Lys Ser His Lys His Pro Lys Thr Val Met Val Glu Asn	
	440 445 450	
40	ATG CGA GCA TAT GAC AAG GGT AAC AGA ACA CGC ATA TTG TTG GGG TCG	1445
	Met Arg Ala Tyr Asp Lys Gly Asn Arg Thr Arg Ile Leu Leu Gly Ser	
	455 460 465	
45	AGG CCT CCG AAT TGT ACA AAC AAA TGT CAT GGT TGC AGT CCA TGT AAG	1493
	Arg Pro Pro Asn Cys Thr Asn Lys Cys His Gly Cys Ser Pro Cys Lys	
	470 475 480	
50	GCC AAG TTA GTT ATT GTT CAT CGT ATT ATG CCG CAG GAG TAT TAT CCT	1541
	Ala Lys Leu Val Ile Val His Arg Ile Met Pro Gln Glu Tyr Tyr Pro	
	485 490 495 500	
55	CAG AGG TGG ATA TGC AGC TGT CAT GGC AAA ATC TAC CAT CCA TAATGAGATA	1593
	Gln Arg Trp Ile Cys Ser Cys His Gly Lys Ile Tyr His Pro	
	505 510	
60	CATTGAAACT GTATGTGCTA GTGAATATTC TTGTGGTACA ATATTAGAAC TGATATTGAA	1653
	AATAAATCAT CAATGTTTCT AAGGCATTTA TAATAGATTA TATTAATGGT TCAGCCTGGT	1713
	GCAAAAAAAA AAA	1726

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 514 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

5	Met	Ala	Met	Lys	Leu	Ile	Ala	Pro	Met	Ala	Phe	Leu	Ala	Met	Gln	Leu
	1				5					10					15	
	Ile	Ile	Met	Ala	Ala	Ala	Glu	Asp	Gln	Ser	Ala	Gln	Ile	Met	Leu	Asp
				20					25					30		
10	Ser	Val	Val	Glu	Lys	Tyr	Leu	Arg	Ser	Asn	Arg	Ser	Leu	Arg	Lys	Val
			35					40					45			
	Glu	His	Ser	Arg	His	Asp	Ala	Ile	Asn	Ile	Phe	Asn	Val	Glu	Lys	Tyr
		50					55					60				
15	Gly	Ala	Val	Gly	Asp	Gly	Lys	His	Asp	Cys	Thr	Glu	Ala	Phe	Ser	Thr
	65					70					75					80
	Ala	Trp	Gln	Ala	Ala	Cys	Lys	Asn	Pro	Ser	Ala	Met	Leu	Leu	Val	Pro
					85					90					95	
20	Gly	Ser	Lys	Lys	Phe	Val	Val	Asn	Asn	Leu	Phe	Phe	Asn	Gly	Pro	Cys
				100					105					110		
	Gln	Pro	His	Phe	Thr	Phe	Lys	Val	Asp	Gly	Ile	Ile	Ala	Ala	Tyr	Gln
25			115					120					125			
	Asn	Pro	Ala	Ser	Trp	Lys	Asn	Asn	Arg	Ile	Trp	Leu	Gln	Phe	Ala	Lys
		130					135					140				
30	Leu	Thr	Gly	Phe	Thr	Leu	Met	Gly	Lys	Gly	Val	Ile	Asp	Gly	Gln	Gly
	145					150					155					160
	Lys	Gln	Trp	Trp	Ala	Gly	Gln	Cys	Lys	Trp	Val	Asn	Gly	Arg	Glu	Ile
35					165					170					175	
	Cys	Asn	Asp	Arg	Asp	Arg	Pro	Thr	Ala	Ile	Lys	Phe	Asp	Phe	Ser	Thr
				180					185					190		
40	Gly	Leu	Ile	Ile	Gln	Gly	Leu	Lys	Leu	Met	Asn	Ser	Pro	Glu	Phe	His
		195						200					205			
	Leu	Val	Phe	Gly	Asn	Cys	Glu	Gly	Val	Lys	Ile	Ile	Gly	Ile	Ser	Ile
		210				215						220				
45	Thr	Ala	Pro	Arg	Asp	Ser	Pro	Asn	Thr	Asp	Gly	Ile	Asp	Ile	Phe	Ala
	225					230					235					240
	Ser	Lys	Asn	Phe	His	Leu	Gln	Lys	Asn	Thr	Ile	Gly	Thr	Gly	Asp	Asp
50					245					250					255	
	Cys	Val	Ala	Ile	Gly	Thr	Gly	Ser	Ser	Asn	Ile	Val	Ile	Glu	Asp	Leu
				260					265					270		
55	Ile	Cys	Gly	Pro	Gly	His	Gly	Ile	Ser	Ile	Gly	Ser	Leu	Gly	Arg	Glu
			275					280					285			
	Asn	Ser	Arg	Ala	Glu	Val	Ser	Tyr	Val	His	Val	Asn	Gly	Ala	Lys	Phe
		290					295					300				
60	Ile	Asp	Thr	Gln	Asn	Gly	Leu	Arg	Ile	Lys	Thr	Trp	Gln	Gly	Gly	Ser
	305					310					315					320
	Gly	Met	Ala	Ser	His	Ile	Ile	Tyr	Glu	Asn	Val	Glu	Met	Ile	Asn	Ser
65					325					330					335	

Glu Asn Pro Ile Leu Ile Asn Gln Phe Tyr Cys Thr Ser Ala Ser Ala
 340 345 350
 5 Cys Gln Asn Gln Arg Ser Ala Val Gln Ile Gln Asp Val Thr Tyr Lys
 355 360 365
 Asn Ile Arg Gly Thr Ser Ala Thr Ala Ala Ala Ile Gln Leu Lys Cys
 370 375 380
 10 Ser Asp Ser Met Pro Cys Lys Asp Ile Lys Leu Ser Asp Ile Ser Leu
 385 390 395 400
 Lys Leu Thr Ser Gly Lys Ile Ala Ser Cys Leu Asn Asp Asn Ala Asn
 405 410 415
 15 Gly Tyr Phe Ser Gly His Val Ile Pro Ala Cys Lys Asn Leu Ser Pro
 420 425 430
 Ser Ala Lys Arg Lys Glu Ser Lys Ser His Lys His Pro Lys Thr Val
 435 440 445
 20 Met Val Glu Asn Met Arg Ala Tyr Asp Lys Gly Asn Arg Thr Arg Ile
 450 455 460
 25 Leu Leu Gly Ser Arg Pro Pro Asn Cys Thr Asn Lys Cys His Gly Cys
 465 470 475 480
 Ser Pro Cys Lys Ala Lys Leu Val Ile Val His Arg Ile Met Pro Gln
 485 490 495
 30 Glu Tyr Tyr Pro Gln Arg Trp Ile Cys Ser Cys His Gly Lys Ile Tyr
 500 505 510
 35 His Pro

(2) INFORMATION FOR SEQ ID NO:135:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:
 50 Arg Lys Val Glu His Ser Arg His Asp Ala Ile Asn Ile Phe Asn Val
 1 5 10 15
 Glu Lys Tyr Gly Ala Val Gly Asp Gly Lys His Asp Cys Thr Glu Ala
 20 25 30
 55 Phe Ser Thr Ala Trp Gln Ala Ala Cys Lys Asn Pro Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO:136:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 65 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Arg Lys Val Glu His Ser Arg His Asp Ala Ile Asn Ile Phe Asn Val
 1 5 10 15
 Glu Lys Tyr Gly Ala Val Gly Asp Gly Lys His Asp Cys Thr Glu Ala
 20 25 30
 Phe Ser Thr Ala Trp Gln Lys Asn Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Ser Arg His Asp Ala Ile Asn Ile Phe Asn Val Glu Lys Tyr Gly Ala
 1 5 10 15
 Val Gly Asp Gly Lys His Asp Cys Thr Glu Ala Phe Ser Thr Ala Trp
 20 25 30
 Gln Lys Asn Pro
 35

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ala Ile Asn Ile Phe Asn Val Glu Lys Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

	AGAAAAGTTG AGCATTCTCG TCATGATGCT ATCAACATCT TCAATGTGGA AAAGTATGGC	60
5	GCAGTAGGCG ATGGAAAGCA TGATTGCACT GAGGCATTTT CAACAGCATG GCAAGCTGCA	120
	TGCAAAAACC CATCAGCAAT GTTGCTTGTG CCAGGCAGCA AGAAATTTGT TGTAACAAT	180
10	CTGTTCTTCA ATGGGCCATG TCAACCTCAC TTTACTTTTA AGGTAGATGG GATAATAGCT	240
	GCGTACCAA ATCCAGCGAG CTGGAAGAAT AATAGAATAT GGTTCAGTT TGCTAACTT	300
	ACAGGTTTTA CTCTAATGGG TAAAGGTGTA ATTGATGGGC AAGGAAAACA ATGGTGGGCT	360
15	GGCCAATGTA AATGGGTCAA TGGACGAGAA ATTTGCAACG ATCGTGATAG ACCAACAGCC	420
	ATTAAATTCG ATTTTCCAC GGGTCTGATA ATCCAAGGAC TGAAACTAAT GAACAGTCCC	480
20	GAATTTTATT TAGTTTTTGG GAATTGTGAG GGAGTAAAA TCATCGGCAT TAGTATTACG	540
	GCACCGAGAG ACAGTCCTAA CACTGATGGA ATTGATATCT TTGCATCTAA AAACTTTCAC	600
	TTACAAAAGA ACACGATAGG AACAGGGGAT GACTGCGTCG CTATAGGCAC AGGGTCTTCT	660
25	AATATTGTGA TTGAGGATCT GATTTGCGGT CCAGGCCATG GAATAAGTAT AGGAAGTCTT	720
	GGGAGGGAAA ACTCTAGAGC AGAGGTTTCA TACGTGCACG TAAATGGGGC TAAATTCATA	780
30	GACACACAAA ATGGATTAAG AATCAAAACA TGGCAGGGTG GTTCAGGCAT GGCAAGCCAT	840
	ATAATTTATG AGAATGTTGA AATGATAAAT TCGGAGAACC CCATATTAAT AAATCAATTC	900
	TACTGCACTT CAGCTTCTGC TTGCCAAAAC CAGAGGTCTG CGGTTCAAAT CCAAGATGTG	960
35	ACATACAAGA ACATACGTGG GACATCAGCA ACAGCAGCAG CAATTCAACT TAAGTGCAGT	1020
	GACAGTATGC CCTGCAAAGA TATAAAGCTA AGTGATATAT CTTTGAAGCT TACCTCAGGG	1080
40	AAAATTGCTT CCTGCCTTAA TGATAATGCA AATGGATATT TCAGTGGACA CGTCATCCCT	1140
	GCATGCAAGA ATTTAAGTCC AAGTGCTAAG CGAAAAGAAT CTAAATCCCA TAAACACCCA	1200
	AAAACGTAA TGGTTGAAAA TATGCGAGCA TATGACAAGG GTAACAGAAC ACGCATATTG	1260
45	TTGGGGTCGA GGCCTCCGAA TTGTACAAAC AAATGTCATG GTTGCAGTCC ATGTAAGGCC	1320
	AAGTTAGTTA TTGTTTCATCG TATTATGCCG CAGGAGTATT ATCCTCAGAG GTGGATATGC	1380
50	AGCTGTCATG GCAAAATCTA CCATCCATAA	1410

(2) INFORMATION FOR SEQ ID NO:140:

55	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1395 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
60	(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

5 TCTCGTCATG ATGCTATCAA CATCTTCAAT GTGGAAAAGT ATGGCGCAGT AGGCGATGGA 60
 AAGCATGATT GCACTGAGGC ATTTTCAACA GCATGGCAAG CTGCATGCAA AAACCCATCA 120
 GCAATGTTGC TTGTGCCAGG CAGCAAGAAA TTTGTTGTAA ACAATCTGTT CTTCAATGGG 180
 10 CCATGTCAAC CTCACTTTAC TTTTAAGGTA GATGGGATAA TAGCTGCGTA CAAAATCCA 240
 GCGAGCTGGA AGAATAATAG AATATGGTTG CAGTTTGCTA AACTTACAGG TTTTACTCTA 300
 ATGGGTAAAG GTGTAATTGA TGGGCAAGGA AAACAATGGT GGGCTGGCCA ATGTAAATGG 360
 15 GTCAATGGAC GAGAAATTTG CAACGATCGT GATAGACCAA CAGCCATTAA ATTTCATTTT 420
 TCCACGGGTC TGATAATCCA AGGACTGAAA CTAATGAACA GTCCCGAATT TCATTTAGTT 480
 TTTGGGAATT GTGAGGGAGT AAAAATCATC GGCATTAGTA TTACGGCACC GAGAGACAGT 540
 20 CCTAACACTG ATGGAATTGA TATCTTTGCA TCTAAAACT TCACTTACA AAAGAACACG 600
 ATAGGAACAG GGGATGACTG CGTCGCTATA GGCACAGGGT CTTCTAATAT TGTGATTGAG 660
 25 GATCTGATTT GCGGTCCAGG CCATGGAATA AGTATAGGAA GTCTTGGGAG GGAAACTCT 720
 AGAGCAGAGG TTTCATACGT GCACGTAAAT GGGGCTAAAT TCATAGACAC ACAAATGGA 780
 TTAAGAATCA AAACATGGCA GGGTGGTTCA GGCATGGCAA GCCATATAAT TTATGAGAAT 840
 30 GTTGAAATGA TAAATTCGGA GAACCCATA TTAATAAATC AATTCTACTG CACTTCAGCT 900
 TCTGCTTGCC AAAACCAGAG GTCTGCGGTT CAAATCCAAG ATGTGACATA CAAGAACATA 960
 35 CGTGGGACAT CAGCAACAGC AGCAGCAATT CAACTTAAGT GCAGTGACAG TATGCCCTGC 1020
 AAAGATATAA AGCTAAGTGA TATATCTTTG AAGCTTACCT CAGGGAAAAT TGCTTCCTGC 1080
 CTTAATGATA ATGCAAATGG ATATTTTCAGT GGACACGTCA TCCCTGCATG CAAGAATTTA 1140
 40 AGTCCAAGTG CTAAGCGAAA AGAATCTAAA TCCCATAAAC ACCCAAAAAC TGTAATGGTT 1200
 GAAAATATGC GAGCATATGA CAAGGGTAAC AGAACACGCA TATTGTTGGG GTCGAGGCCT 1260
 45 CCGAATTGTA CAAACAAATG TCATGGTTGC AGTCCATGTA AGGCCAAGTT AGTTATTGTT 1320
 CATCGTATTA TGCCGCAGGA GTATTATCCT CAGAGGTGGA TATGCAGCTG TCATGGCAAA 1380
 ATCTACCATC CATAA 1395

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 1479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAAGATCAAT CTGCCCAAAT TATGTTGGAC AGTGTGTGCG AAAAAATATCT TAGATCGAAT 60

CGGAGTTTAA GAAAAGTTGA GCATTCTCGT CATGATGCTA TCAACATCTT CAATGTGGAA 120
 AAGTATGGCG CAGTAGGCGA TGGAAAGCAT GATTGCACTG AGGCATTTTC AACAGCATGG 180
 5 CAAGCTGCAT GCAAAAACCC ATCAGCAATG TTGCTTGTC CAGGCAGCAA GAAATTTGTT 240
 GTAAACAATC TGTTCCTCAA TGGGCCATGT CAACCTCACT TTACTTTTAA GGTAGATGGG 300
 10 ATAATAGCTG CGTACCAAAA TCCAGCGAGC TGAAGAATA ATAGAATATG GTTGCAGTTT 360
 GCTAAACTTA CAGGTTTTAC TCTAATGGGT AAAGGTGTAA TTGATGGGCA AGGAAAACAA 420
 TGGTGGGCTG GCCAATGTAA ATGGGTCAAT GGACGAGAAA TTTGCAACGA TCGTGATAGA 480
 15 CCAACAGCCA TTAAATTCGA TTTTTCACG GGTCTGATAA TCCAAGGACT GAAACTAATG 540
 AACAGTCCCG AATTTTCATTT AGTTTTTGGG AATTGTGAGG GAGTAAAAAT CATCGGCATT 600
 AGTATTACGG CACCGAGAGA CAGTCCTAAC ACTGATGGAA TTGATATCTT TGCATCTAAA 660
 20 AACTTTTCACT TACAAAAGAA CACGATAGGA ACAGGGGATG ACTGCGTCGC TATAGGCACA 720
 GGGTCTTCTA ATATTGTGAT TGAGGATCTG ATTTGCGGTC CAGGCCATGG AATAAGTATA 780
 25 GGAAGTCTTG GGAGGGAAAA CTCTAGAGCA GAGGTTTCAT ACGTGCACGT AAATGGGGCT 840
 AAATTCATAG ACACACAAAA TGGATTAAGA ATCAAAACAT GGCAGGGTGG TTCAGGCATG 900
 GCAAGCCATA TAATTTATGA GAATGTTGAA ATGATAAATT CGGAGAACCC CATATTAATA 960
 30 AATCAATTCT ACTGCACTTC AGCTTCTGCT TGCCAAAACC AGAGGTCTGC GGTTCAAATC 1020
 CAAGATGTGA CATACAAGAA CATACTGGG ACATCAGCAA CAGCAGCAGC AATTCAACTT 1080
 35 AAGTGCAGTG ACAGTATGCC CTGCAAAGAT ATAAAGCTAA GTGATATATC TTTGAAGCTT 1140
 ACCTCAGGGA AAATTGCTTC CTGCCTTAAT GATAATGCAA ATGGATATTT CAGTGGACAC 1200
 GTCATCCCTG CATGCAAGAA TTTAAGTCCA AGTGCTAAGC GAAAAGAATC TAAATCCCAT 1260
 40 AAACACCCAA AAAGTGAAT GGTTGAAAAT ATGCGAGCAT ATGACAAGGG TAACAGAACA 1320
 CGCATATTGT TGGGGTCGAG GCCTCCGAAT TGTACAAACA AATGTCATGG TTGCAGTCCA 1380
 45 TGTAAGGCCA AGTTAGTTAT TGTTCATCGT ATTATGCCGC AGGAGTATTA TCCTCAGAGG 1440
 TGGATATGCA GCTGTCATGG CAAAATCTAC CATCCATAA 1479

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

RTAYTTYTCN ACRTTRAA

18

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Phe Asn Val Glu Lys Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CCTGCAGTAY TTYTCNACRT TRAANAT

27

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CCTGCAG

7

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Ile Phe Asn Val Glu Lys Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

5 CCTGCAGTAY TTYTCNACRT TRAADAT

27

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

20 GCNATHAAYA THTTYAA

17

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

35 Ala Ile Asn Ile Phe Asn
1 5

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

50 GGAATTCCGC NATHAAYATH TTYAAYGT

28

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GGAATTCC

8

65 (2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
5
(ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
10
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:
 Ala Ile Asn Ile Phe Asn Val
 1 5

15 (2) INFORMATION FOR SEQ ID NO:153:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA
25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:
 GCYTCNGTRC ARTCRTGYTT

20

30 (2) INFORMATION FOR SEQ ID NO:154:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
35 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:
 Lys His Asp Cys Thr Glu Ala
 1 5

45 (2) INFORMATION FOR SEQ ID NO:155:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:
 GGCTGCAGGT RCARTCRTGY TTNCCRTC

28

60 (2) INFORMATION FOR SEQ ID NO:156:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 base pairs
 (B) TYPE: nucleic acid
65 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

5 GGCTGCAG

8

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

15

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

20

Asp Gly Lys His Asp Cys Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

35

ATGTTGGACA GTGTTGTCGA A

21

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

45

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

50

GGGAATTCAG AAAAGTTGAG CATTCTCGT

29

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: cDNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GGGAATTC

8

65

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:
10 GTTCTTCAAT GGGCCATGT 19

(2) INFORMATION FOR SEQ ID NO:162:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:
25 GTGTTAGGAC TGTCTCTCGG 20

(2) INFORMATION FOR SEQ ID NO:163:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:
40 TGTCCAGGCC ATGGAATAAG 20

(2) INFORMATION FOR SEQ ID NO:164:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:
55 GCCTTACATG GACTGCAACC 20

(2) INFORMATION FOR SEQ ID NO:165:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

TCCACGGGTC TGATAATCCA

20

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

AGGCAGGAAG CAATTTTCCC

20

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

TACTGCACTT CAGCTTCTGC

20

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGGGGTCTCC GAATTTATCA

20

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GGATATTTCA GTGGACACGT

20

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TATTAGAAGA CCCTGCGCCT

20

10

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CCATGTAAGG CCAAGTTAGT

20

25

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: cDNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

ACACCTTTAC CCATTAGAGT

20

40

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: cDNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CTGTCCAACA TAATTTGGGC

20

55

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CATGGCAGGG TGGTTCAGGC

20

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

TAGCCCCATT TACGTGCACG

20

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TTGGGGTCGA GGCCTCCGAA

20

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

TAAAAUGGC

9

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AACAAUGGC

9

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GCCGAATTCA TGGCCATGAA ATTAATT

27

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GCCGAATTC

9

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CGGGGATCCT CATTATGGAT GGTAGAT

27

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CGGGGATCC

9

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Phe Thr Phe Lys Val Asp Gly Ile Ile Ala Ala Tyr Gln
1 5

10

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asn Gly Tyr Phe Ser Gly His Val Ile Pro Ala Cys Lys Asn
1 5

10

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Phe Thr Phe Lys Val Asp Gly Ile Ile Ala Ala Tyr Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Asn Gly Tyr Phe Ser Gly His Val Ile Pro Ala Cys Lys Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Gly His His His His His His Glu Phe Arg Lys Val Glu His Ser
 1 5 10 15
 Arg His Asp Ala Ile Asn Ile Phe Asn Val Glu Lys Tyr Gly Ala Val
 20 25 30
 Gly Asp Gly Lys His Asp Cys Thr Glu Ala Phe Ser Thr Ala Trp Gln
 35 40 45
 Ala Ala Cys Lys Asn Pro Ser Ala Met Leu Leu Val Pro Gly Ser Lys
 50 55 60
 Lys Phe Val Val Asn Asn Leu Phe Phe Asn Gly Pro Cys Gln Pro His
 65 70 75 80
 Phe Thr Phe Lys Val Asp Gly Ile Ile Ala Ala Tyr Gln Asn Pro Ala
 85 90 95
 Ser Trp Lys Asn Asn Arg Ile Trp Leu Gln Phe Ala Lys Leu Thr Gly
 100 105 110
 Phe Thr Leu Met Gly Lys Gly Val Ile Asp Gly Gln Gly Lys Gln Trp
 115 120 125

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Met Gly His His His His His His Glu Phe Trp Ala Gly Gln Cys Lys
 1 5 10 15
 Trp Val Asn Gly Arg Glu Ile Cys Asn Asp Arg Asp Arg Pro Thr Ala
 20 25 30
 Ile Lys Phe Asp Phe Ser Thr Gly Leu Ile Ile Gln Gly Leu Lys Leu
 35 40 45
 Met Asn Ser Pro Glu Phe His Leu Val Phe Gly Asn Cys Glu Gly Val
 50 55 60
 Lys Ile Ile Gly Ile Ser Ile Thr Ala Pro Arg Asp Ser Pro Asn Thr
 65 70 75 80
 Asp Gly Ile Asp Ile Phe Ala Ser Lys Asn Phe His Leu Gln Lys Asn
 85 90 95
 Thr Ile Gly Thr Gly Asp Asp Cys Val Ala Ile Gly Thr Gly Ser Ser
 100 105 110
 Asn Ile Val Ile Glu Asp Leu Ile Cys Gly Pro Gly His Gly Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

10 Met Gly His His His His His His Glu Phe Ser Ile Gly Ser Leu Gly
 1 5 10 15
 15 Arg Glu Asn Ser Arg Ala Glu Val Ser Tyr Val His Val Asn Gly Ala
 20 25 30
 Lys Phe Ile Asp Thr Gln Asn Gly Leu Arg Ile Lys Thr Trp Gln Gly
 35 40 45
 20 Gly Ser Gly Met Ala Ser His Ile Ile Tyr Glu Asn Val Glu Met Ile
 50 55 60
 Asn Ser Glu Asn Pro Ile Leu Ile Asn Gln Phe Tyr Cys Thr Ser Ala
 65 70 75 80
 25 Ser Ala Cys Gln Asn Gln Arg Ser Ala Val Gln Ile Gln Asp Val Thr
 85 90 95
 Tyr Lys Asn Ile Arg Gly Thr Ser Ala Thr Ala Ala Ala Ile Gln Leu
 100 105 110
 30 Lys Cys Ser Asp Ser Met Pro Cys Lys Asp Ile Lys Leu Ser Asp
 115 120 125

35 (2) INFORMATION FOR SEQ ID NO:190:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

50 Met Gly His His His His His His Glu Phe Ile Ser Leu Lys Leu Thr
 1 5 10 15
 Ser Gly Lys Ile Ala Ser Cys Leu Asn Asp Asn Ala Asn Gly Tyr Phe
 20 25 30
 55 Ser Gly His Val Ile Pro Ala Cys Lys Asn Leu Ser Pro Ser Ala Lys
 35 40 45
 Arg Lys Glu Ser Lys Ser His Lys His Pro Lys Thr Val Met Val Glu
 50 55 60
 60 Asn Met Arg Ala Tyr Asp Lys Gly Asn Arg Thr Arg Ile Leu Leu Gly
 65 70 75 80

Ser Arg Pro Pro Asn Cys Thr Asn Lys Cys His Gly Cys Ser Pro Cys
85 90 95

Lys Ala Lys Leu Val Ile Val His Arg Ile Met Pro Gln Glu Tyr Tyr
100 105 110

Pro Gln Arg Trp Ile Cys Ser Cys His Gly Lys Ile Tyr His Pro
115 120 125

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Gly Lys Gly Val Ile Asp Gly Gln Gly Lys Gln Trp Trp Ala Gly Gln
1 5 10 15

Cys Lys Trp Val Asn Gly Arg Glu
20

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Asp Ser Met Pro Cys Lys Asp Ile Lys Leu Ser Asp Ile Ser Leu Lys
1 5 10 15

Leu Thr Ser Gly Lys Ile Ala Ser
20

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Ile Glu Asp Leu Ile Cys Gly Pro Gly His Gly Ile Ser Ile Gly Ser
 1 5 10 15

Leu Gly Arg Glu Asn Ser Arg Ala
 20

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

MOLECULE TYPE: cDNA

(ii)

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 6, 15
- (D) OTHER INFORMATION: /mod_base= i

SEQUENCE DESCRIPTION: SEQ ID NO:194:

(xi)

AAYCCNATHG AYWSNCGYTG G

21

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

AAYTGGGCNC ARAAYRGNAT GAA

23

A3
(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGCGGATCCT TACCATTGTT TTCCTTGCCC

30

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CGGGAATTCT GGGCTGGCCA ATGTAAA

27

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GGCGGATCCT TATATTCCAT GGCCTGGACC

30

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

A4
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

CGGGAATTCA GTATAGGAAG TCTTGGG

27

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GGCGGATCCT TAATCACTTA GCTTTATATC

30

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CGGGAATTCA TATCTTTGAA GCTTACC

27